(a) mixing at least one random primer at least 4 nucleotides in length and having at least one detectable species with a sample which may contain nucleic acid contamination to form a mixture;

(b) adding at least one nucleotide triphosphate having at least one binding species and optionally at least one second nucleotide triphosphate to the mixture;

(c) adding at least one nucleic acid polymerase to the mixture;

(d) incubating the mixture of step (c) under conditions which allow said at least one nucleic acid polymerase to be active;

(e) contacting the mixture of step (d) with at least one solid phase; and

(f) measuring the amount of total nucleic acid contamination in the sample by measuring the total amount of said at least one detectable species bound to said solid phase.

E2 cont.

42. (New) A method for determining the amount of total nucleic acid contamination in a sample, said method comprising:

(a) mixing at least one random primer at least 4 nucleotides in length and having at least one binding species with a sample which may contain nucleic acid contamination to form a mixture;

(b) adding at least one nucleotide triphosphate having at least one detectable species and optionally at least one second nucleotide triphosphate to the mixture;

(c) adding at least one nucleic acid polymerase to the mixture;

(d) incubating the mixture of step (c), under conditions which allow said at least one nucleic acid polymerase to be active;

(e) contacting the mixture of step (d) with at least one solid phase; and

(f) measuring the amount of total nucleic acid contamination in the sample by measuring the total amount of said at least one detectable species bound to said solid phase.

43. (New) A method for determining the amount of total nucleic acid contamination in ae sample, said method comprising:

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(a) mixing at least one random primer at least 4 nucleotides in length with a sample which may contain nucleic acid contamination to form a mixture;

(b) adding at least one nucleotide triphosphate having at least one detectable species and optionally at least one nucleotide triphosphate having at least one detectable species and optionally at least one second nucleotide triphosphate to the mixture;

(c) adding at least one nucleic acid polymerase to the mixture;

(d) incubating the mixture of step (c), under conditions which allow said at least one nucleic acid polymerase to be active;

(e) contacting the mixture of step (d) with at least one solid phase; and

(f) measuring the amount of total nucleic acid contamination in the sample by measuring the total amount of said at least one detectable species or the total amount of said at least one binding species bound to said solid phase.

E2 cont.

~~44~~. (New) A method for determining the amount of total nucleic acid contamination in a sample, said method comprising:

(a) mixing at least one first labeled random primer at least 4 nucleotides in length having at least one binding species and at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid contamination to form a mixture;

(b) adding at least one nucleic acid ligase to the mixture;

(c) incubating the mixture of step (b), under conditions which allow said at least one nucleic acid ligase to be active;

(d) contacting the mixture of step (c) with at least one solid phase; and

(e) measuring the amount of total nucleic acid contamination in the sample by measuring the total amount of said at least one detectable species or the total amount of said at least one binding species bound to said solid phase.

~~45~~. (New) A method for determining the amount of total nucleic acid contamination in a sample, said method comprising:

(a) mixing at least one first labeled random primer at least 4 nucleotides in length having at least one binding species and at least one second random primer at least 4 nucleotides in length having at least one detectable species, with a sample which may contain nucleic acid contamination to form a mixture;

(b) adding at least one nucleic acid ligase and at least one nucleic acid polymerase to the mixture;

(c) incubating the mixture of step (b), under conditions which allow said at least one nucleic acid ligase and said nucleic acid polymerase to be active;

(d) contacting the mixture of step (c) with at least one solid phase; and

(e) measuring the amount of total nucleic acid contamination in the sample by measuring the total amount of said at least one detectable species or the total amount of said at least one binding species bound to said solid phase.

E2 cont.

46. (New) A method as in claim 41, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, T4 DNA polymerase, Klenow fragment, Pfu DNA polymerase, Exo- Pfu DNA polymerase, E. coli DNA polymerase I, Klenow fragment of DNA polymerase I, MMLV reverse transcriptase and AMV reverse transcriptase.

47. (New) A method as in claim 41, wherein said conditions comprise a solution with a pH between 5.5 and 9.5, a nucleotide triphosphate concentration between 1 pM and 10 mM, a Mg2+ concentration between 0.05 mM and 500 mM, and a reducing agent concentration between 0 and 500 mM, wherein the sum of the molarities is between 1 mM and 500 mM.

48. (New) A method as in claim 44, wherein said at least one ligase is selected from the group consisting of Pfu DNA ligase, T4 DNA ligase, Taq DNA ligase, T4 RNA ligase, and E. coli DNA ligase.

49. (New) A method as in claim 41, wherein said random primer is from 4 to 20 nucleotides in length.

50. (New) A method as in claim 49, wherein said at least one detectable species is selected from the group consisting of biotin, nucleic acid sequence, nucleic acid base pairing linear polymer, fluorescent molecule, electrochemiluminescent molecule, radioactive molecule, peroxidase and alkaline phosphatase.

51. (New) A method as in claim 49, wherein said at least one binding species is selected from the group consisting of biotin, antigen, lectin, ligand, hormone, nucleic acid sequence, mimitope and nucleic acid base pairing linear polymer.

52. (New) A method as in claim 49, wherein said at least one nucleic acid polymerase is selected from the group consisting of Taq DNA polymerase, Klenow fragment (3'-5') of E. coli DNA polymerase I and Klenow fragment of DNA polymerase I.

53. (New) A method as in claim 49, wherein said at least one solid phase is selected from the group consisting of magnetic bead, plastic plate and polymer bead.

54. (New) A method as in claim 49, wherein said at least one nucleotide triphosphate is selected from the group consisting of dATP, dGTP, dCTP, dUTP, dTTP, 7-deaza dGTP, biotin-dATP, biotin-dCTP, biotin-dUTP, digoxigenin dUTP, digoxigenin UTP and biotin ddUTP.

55. (New) A method as in claim 49, wherein said random primer is 6-10 nucleotides in length.

56. (New) A method as in claim 49, wherein said conditions comprise those optimal for Klenow fragment of DNA polymerase I to synthesize DNA.

57. (New) A method as in claim 56, wherein said NTP is a dNTP.

58. (New) The method of claim 41, wherein said total amount of nucleic acid contamination comprises two or more different nucleic acid species of unknown sequence.

59. (New) The method of claim 41, wherein said total amount of nucleic acid contamination comprises double and single-stranded nucleic acid sequences.

60. (New) The method of claim 41, wherein said total amount of nucleic acid contamination comprises DNA, RNA or combinations thereof.

61. (New) The method of claim 58, wherein said nucleic acid species are larger than 100 bases.